

241421.txt  
SEQUENCE LISTING

<110> Sewalt, Vincent  
Hastings, Craig  
Meeley, Robert  
Hantke, Sabine  
Jung, Rudolf  
Everard, John  
Allen, Stephen

<120> COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PROTEINS

<130> 5718-119 (035718/241421)

<150> 60/250,703  
<151> 2000-12-01

<160> 25

<170> PatentIn version 3.0

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<213> Zea mays

<220>  
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<222> (187)..(573)

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tgattatttc taggaaacac atgccggaat gagggcacca ttatccgcgt ccagtgtgtc  
120

cgctactccg ctccccctca gtcctcagtt cctcacctag cggttagcgtg cgccgcggag  
180

acgttag atg gcg gct tcg gag gcg gca gcg gcg gca aca ccg gtg  
228

Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Ala Thr Pro Val  
1 5 10

acg ccg aca gag ggg acg gtg atc gcg atc cac agc ctg gag gag tgg  
276

Thr Pro Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp  
15 20 25 30

agc atc cag atc gag gag gcc aac agc gcc aag aag ctg gtg gtg att  
324  
Ser Ile Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile  
35 40 45

gac ttc act gca aca tgg tgt cct ccg tgc cgc gcc atg gct cca att  
372  
Asp Phe Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile

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50

55

60

ttt gct gat atg gcc aag aag tcc cca aat gtt gtt ttc ctg aaa gtt  
 420  
 Phe Ala Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val  
 65 70 75

gat gtg gat gaa atg aag acc att gct gag caa ttc agc gta gag gcc  
 468  
 Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala  
 80 85 90

atg cca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc  
 516  
 Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val  
 95 100 105 110

gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg  
 564  
 Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met  
 115 120 125

gcc tcg tag atcagtgtatcgccgtatcgctaaataagagg  
 613  
 Ala Ser

acgcctcgcc tcaactctga gaaaactagt gcttctgtga tggtaattcg tatgagagag  
 673

tgcgcgcgttt ggtggtaactt cttcgtatgt agtattaact cctgtcttaa tatgttgccc  
 733

tgcttgcgtttttcataccatgtttgtcttttcagctgag gtgttaaaaa aaaaaaaaaa  
 793

aaaa  
 797

<210> 2  
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<400> 2

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 1 5 10 15

Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile  
 20 25 30

Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe  
 35 40 45

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Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile Phe Ala  
 50 55 60

Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val Asp Val  
 65 70 75 80

Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala Met Pro  
 85 90 95

Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val Val Gly  
 100 105 110

Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met Ala Ser  
 115 120 125

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<220>  
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 60

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 110  
 Met Ala Ala Ser Ala Ala Ala Ala Ala Thr Pro Val  
 1 5 10

gcg ccg aca gag ggg acg gtg atc gcg atc cac agc ctg gag gag tgg  
 158  
 Ala Pro Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp  
 15 20 25 30

agc atc cag atc gag gag gcc aac agc gcc aag aag ctg gtg gtg att  
 206  
 Ser Ile Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile  
 35 40 45

gac ttc act gca aca tgg tgt cct ccg tgc cgc gcc atg gct cca att  
 254  
 Asp Phe Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile  
 50 55 60

ttt gct gat atg gcc aag aag tcc cca aat gtt gtt ttc ctg aaa gtt  
 302  
 Phe Ala Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val  
 65 70 75

gat gtc gat gaa atg aag acc att gct gag caa ttc agc gta gag gcc

350  
 Asp Val Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala  
 80 85 90

atg cca aca ttc ctg ttc atg agg gag ggc gac gtc aag gac agg gtc  
 398  
 Met Pro Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val  
 95 100 105 110

gtt ggc gca gca aag gaa gag cta gca agg aag ctt gaa cta cac atg  
 446  
 Val Gly Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met  
 115 120 125

gcc tcg tag atcagtgtatg ccgtaatgta gtattcgctt aaataagagg  
 495  
 Ala Ser

acgcctcgcc tcaactctga gaaaactagt gcttctgtga tggtaattcg tatgagagag  
 555

tgcccccttt ggtggtaactt cttcgtatgt agtattaact cctgtcttaa tatgttgc  
 615

tgcttgcgt tttcataccca tgtttgctct ttcagctgag gtgttatacg gtaaatcgga  
 675

gtcaatatct ttgaaattga ttaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa  
 735

aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa  
 795

aaaaa  
 799

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 <211> 128  
 <212> PRT  
 <213> Zea mays

<400> 4

Met Ala Ala Ser Glu Ala Ala Ala Ala Ala Ala Thr Pro Val Ala Pro  
 1 5 10 15

Thr Glu Gly Thr Val Ile Ala Ile His Ser Leu Glu Glu Trp Ser Ile  
 20 25 30

Gln Ile Glu Glu Ala Asn Ser Ala Lys Lys Leu Val Val Ile Asp Phe  
 35 40 45

Thr Ala Thr Trp Cys Pro Pro Cys Arg Ala Met Ala Pro Ile Phe Ala  
 50 55 60

Asp Met Ala Lys Lys Ser Pro Asn Val Val Phe Leu Lys Val Asp Val  
 65 70 75 80

Asp Glu Met Lys Thr Ile Ala Glu Gln Phe Ser Val Glu Ala Met Pro  
 85 90 95

Thr Phe Leu Phe Met Arg Glu Gly Asp Val Lys Asp Arg Val Val Gly  
 100 105 110

Ala Ala Lys Glu Glu Leu Ala Arg Lys Leu Glu Leu His Met Ala Ser  
 115 120 125

<210> 5  
 <211> 367  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (3)..(194)

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 47 Arg Phe Ser Asp Ala Ile Phe Val Lys Val Asp Val Asp Glu Leu  
 1 5 10 15

gag gtc gca agg aca tgg aag gta gag gcg atg cca acg ttc gta  
 95 Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val  
 20 25 30

ctt gtc aag gat ggg aag gag gta agc cgt gtg gtt ggg gcc aag aag  
 143 Leu Val Lys Asp Gly Lys Glu Val Ser Arg Val Val Gly Ala Lys Lys  
 35 40 45

gac gag ctt gag agg aag atc cgg atg ttc acg tca tct tcc tca tcg  
 191 Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Thr Ser Ser Ser Ser  
 50 55 60

taa actcctgtgg ttgcgcgtgg acggagttgc tgaagtggaaa tggcccttc  
 244

tctcaatgct gaaaaaaggg gaaaaaacta tgtgaaaatg atggtagacg tgtctgggtc  
 304

agtaataaga gtttctaaaa tctgaatgag atttgaatcg ctttccgttg ctgaaaaaaaa  
 364

aaa  
 367

<210> 6  
<211> 63  
<212> PRT  
<213> Zea mays

<400> 6

Arg Phe Ser Asp Ala Ile Phe Val Lys Val Asp Val Asp Glu Leu Ala  
1 5 10 15

Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu  
20 25 30

Val Lys Asp Gly Lys Glu Val Ser Arg Val Val Gly Ala Lys Lys Asp  
35 40 45

Glu Leu Glu Arg Lys Ile Arg Met Phe Thr Ser Ser Ser Ser  
50 55 60

<210> 7  
<211> 720  
<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (38)..(442)

<400> 7  
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55 Met Gly Ser Phe Phe Ser  
1 5

acc tta gtg acg ccc cct ccg ccc gcc gac gac ccg aac tgc gcc  
103  
Thr Leu Val Thr Pro Pro Pro Ala Ala Asp Asp Pro Asn Cys Ala  
10 15 20

gtg gtg gcc gcg cac tcc aag gcc acc tac gac gag cag tgg gcg gcc  
151  
Val Val Ala Ala His Ser Lys Ala Thr Tyr Asp Glu Gln Trp Ala Ala  
25 30 35

cac aag agc agc agc aag ctg atg gtg atc gac ttc tcg gcg tcc tgg  
199  
His Lys Ser Ser Ser Lys Leu Met Val Ile Asp Phe Ser Ala Ser Trp  
40 45 50

tgc ggg ccc tgc cgc ttc atc gag ccg gcc ttc aag gag ctg gcc tcc  
247  
Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala Phe Lys Glu Leu Ala Ser  
55 60 65 70

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cgc ttc acc gat gcc atc ttc atc aag gtc gac gtc gac gag ctc gcg  
295  
Arg Phe Thr Asp Ala Ile Phe Ile Lys Val Asp Val Asp Glu Leu Ala  
75 80 85

gag gtc gca agg aca tgg aag gta gag gcg atg cca acg ttc gtg ctg  
343  
Glu Val Ala Arg Thr Trp Lys Val Glu Ala Met Pro Thr Phe Val Leu  
90 95 100

gtc aag gat ggg aag gag gta ggc cgt gtg att ggg gct aag aag gac  
391  
Val Lys Asp Gly Lys Glu Val Gly Arg Val Ile Gly Ala Lys Lys Asp  
105 110 115

gag ctt gag agg aag atc agg atg ttc gtc acg tca tct tcc tcg tcc  
439  
Glu Leu Glu Arg Lys Ile Arg Met Phe Val Thr Ser Ser Ser Ser  
120 125 130

taa ctttagcagtg catacactcc caccttatta ctggtttctc gactccagtg  
492

gttcgcctgg gacggggttg ctgaaatggt tcccttctct gaataactgaa aaatcaaaaa  
552

aagaagtata tgaaaaaaatg atggtagacg tgtctggtc aataagagtt tctgaaactt  
612

ggatttgtat gtgtcagtct ctgtgttctg tttccaagga atggatcatg tgagtttgg  
672

atatagctgg aaatatgttg tgctgttaaa aaaaaaaaaa aaaaaaaaaa  
720

<210> 8  
<211> 134  
<212> PRT  
<213> Zea mays

<400> 8

Met Gly Ser Phe Phe Ser Thr Leu Val Thr Pro Pro Pro Pro Ala Ala  
1 5 10 15

Asp Asp Pro Asn Cys Ala Val Val Ala Ala His Ser Lys Ala Thr Tyr  
20 25 30

Asp Glu Gln Trp Ala Ala His Lys Ser Ser Ser Lys Leu Met Val Ile  
35 40 45

Asp Phe Ser Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Glu Pro Ala  
50 55 60

241421.txt

Phe Lys Glu Leu Ala Ser Arg Phe Thr Asp Ala Ile Phe Ile Lys Val  
65 70 75 80

Asp Val Asp Glu Leu Ala Glu Val Ala Arg Thr Trp Lys Val Glu Ala  
85 90 95

Met Pro Thr Phe Val Leu Val Lys Asp Gly Lys Glu Val Gly Arg Val  
100 105 110

Ile Gly Ala Lys Lys Asp Glu Leu Glu Arg Lys Ile Arg Met Phe Val  
115 120 125

Thr Ser Ser Ser Ser Ser  
130

<210> 9  
<211> 722  
<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (84)..(455)

<400> 9  
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60

ccaccgagga agaagagaga gga atg gcg tcc gag gag gaa gga gtc gtg atc  
113  
Met Ala Ser Glu Glu Gly Val Val Ile  
1 5 10

gcc tgc cac acc aag gcc gac ttc gac gcc cac atg gcc aag gcc aag  
161  
Ala Cys His Thr Lys Ala Asp Phe Asp Ala His Met Ala Lys Ala Lys  
15 20 25

gag gcc ggc aag ctg gtg atc att gac ttc acg gcc tcc tgg tgc ggc  
209  
Glu Ala Gly Lys Leu Val Ile Ile Asp Phe Thr Ala Ser Trp Cys Gly  
30 35 40

ccc tgc cgc ttc atc gcg cca ctg ttc gtc gag cac gcc aag aag ttc  
257  
Pro Cys Arg Phe Ile Ala Pro Leu Phe Val Glu His Ala Lys Lys Phe  
45 50 55

acc cag gct gtg ttc ctg aag gtg gac gtg gac gag ctg aag gaa gtt  
305  
Thr Gln Ala Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Glu Val  
60 65 70

241421.txt

gcc gcg gcc tac gat gtc gag gcg atg ccg acc ttc cac ttc gtc aag  
353  
Ala Ala Ala Tyr Asp Val Glu Ala Met Pro Thr Phe His Phe Val Lys  
75 80 85 90

aac ggg gtg acg gtc gag acc gtc gtc ggt gcc agg aag gag aac ctc  
401  
Asn Gly Val Thr Val Glu Thr Val Val Gly Ala Arg Lys Glu Asn Leu  
95 100 105

ctg gcc cag atc gag aag cac tgc gcc gcg gcc gtg cct gct gcg tct  
449  
Leu Ala Gln Ile Glu Lys His Cys Ala Ala Ala Val Pro Ala Ala Ser  
110 115 120

gcg tag agaggatgga ccagcacgtg gcgggtggcgg tggcggttgt cttgtcggtt  
505  
Ala

tcagtttggg cttgtcagct gtggctgggt ggttggattgt gaactggagc atgcagtttt  
565

actctgggag cccatcattt ggttggctca ggtgtcaata atctgtatac cttaatcatg  
625

gatagttgtt gtgagttgtt attggacttt ggaatttggaa tgtctggctt cgttctgtta  
685

tgtatgtatgat gatggattga aaaaaaaaaa aaaaaaaaa  
722

<210> 10  
<211> 123  
<212> PRT  
<213> Zea mays  
  
<400> 10

Met Ala Ser Glu Glu Glu Gly Val Val Ile Ala Cys His Thr Lys Ala  
1 5 10 15

Asp Phe Asp Ala His Met Ala Lys Ala Lys Glu Ala Gly Lys Leu Val  
20 25 30

Ile Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala  
35 40 45

Pro Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Ala Val Phe Leu  
50 55 60

Lys Val Asp Val Asp Glu Leu Lys Glu Val Ala Ala Ala Tyr Asp Val  
65 70 75 80

241421.txt

Glu Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Val Thr Val Glu  
85 90 95

Thr Val Val Gly Ala Arg Lys Glu Asn Leu Leu Ala Gln Ile Glu Lys  
100 105 110

His Cys Ala Ala Ala Val Pro Ala Ala Ser Ala  
115 120

<210> 11  
<211> 727  
<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (84)..(452)

<400> 11  
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cgacaccgag gaagaagaga tca atg gcg tcc gag cag gga gtc gtg atc gcg  
113  
Met Ala Ser Glu Gln Gly Val Val Ile Ala  
1 5 10

tgc cac agc aag gct gag ttt gac gcc cac atg acc aag gcc cag gaa  
161  
Cys His Ser Lys Ala Glu Phe Asp Ala His Met Thr Lys Ala Gln Glu  
15 20 25

gcc ggc aag ctg gtg gtc att gac ttc act gcc gcc tgg tgc ggt cca  
209  
Ala Gly Lys Leu Val Val Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro  
30 35 40

tgc cgc gcc atc gcc cca ctg ttc gtc gaa cac gcc aag aag ttc act  
257  
Cys Arg Ala Ile Ala Pro Leu Phe Val Glu His Ala Lys Lys Phe Thr  
45 50 55

cag gtc gtc ttc ctg aag gtg gac gtg gac gaa gtg aag gaa gtc acc  
305  
Gln Val Val Phe Leu Lys Val Asp Val Asp Glu Val Lys Glu Val Thr  
60 65 70

gcg gcc tac gag gtc gag gcg atg ccg acc ttc cac ttc gtc aag aac  
353  
Ala Ala Tyr Glu Val Glu Ala Met Pro Thr Phe His Phe Val Lys Asn  
75 80 85 90

ggc aag acg gtc gcg acc atc gtg ggt gcc aag aag gac gag ctc ctg  
401  
Gly Lys Thr Val Ala Thr Ile Val Gly Ala Lys Lys Asp Glu Leu Leu

95

100

105

gcc cag atc gag aag cat gcc gcg cct gcg cct gcg tct gcg tct gcc  
 449  
 Ala Gln Ile Glu Lys His Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala  
 110 115 120

taa aggagatcatc atcagtcgtc gccgtcaata agggccagca cgtatggctg  
 502

taaatgttgtt cgttatcagt tctggctttg tcgtttgtgg gcgattgtga actagtagta  
 562

tgtttgtttc tatccgagcc ggaggcgata cttaaccatg gatacttgtt gtgagttcgt  
 622

ttctgttcgc gtgtgactct tgaattgaat caaccagctc accactgcac cagggccgtgg  
 682

tgagtggta cagtgatttc ctgttaaaaa aaaaaaaaaa aaaaa  
 727

<210> 12  
 <211> 122  
 <212> PRT  
 <213> Zea mays

<400> 12

Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu  
 1 5 10 15

Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val  
 20 25 30

Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro  
 35 40 45

Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys  
 50 55 60

Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu  
 65 70 75 80

Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr  
 85 90 95

Ile Val Gly Ala Lys Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His  
 100 105 110

Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala

115

120

<210> 13  
 <211> 700  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (41)..(421)

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 Met Ala Ala Glu Glu  
 1 5

ggc gcc atc ggc tgc cac acc aag gac gag ttc gac gcc cgc atg  
 103  
 Gly Ala Val Ile Ala Cys His Thr Lys Asp Glu Phe Asp Ala Arg Met  
 10 15 20

gcc aag gcc aag gag cag ggc aag ctg gtg gtc atc gac ttc atg gcc  
 151  
 Ala Lys Ala Lys Glu Gln Gly Lys Leu Val Val Ile Asp Phe Met Ala  
 25 30 35

ccc tgg tgc agt ggg tgc cag atg atg gcc ccg gtg tac gcg gac tgc  
 199  
 Pro Trp Cys Ser Gly Cys Gln Met Met Ala Pro Val Tyr Ala Asp Cys  
 40 45 50

gcc agc aag tac cct tcc gcg gtc ttc ctc gag gtc gac gtc gac gaa  
 247  
 Ala Ser Lys Tyr Pro Ser Ala Val Phe Leu Glu Val Asp Val Asp Glu  
 55 60 65

ctg ctg gaa gtc gcg aag atc tac ggc gtc cat gtg atg ccg acc ttc  
 295  
 Leu Leu Glu Val Ala Lys Ile Tyr Gly Val His Val Met Pro Thr Phe  
 70 75 80 85

tgc ttc atc agg aac ggc gag acg ctc gag agc ttt gct acc gtc gac  
 343  
 Cys Phe Ile Arg Asn Gly Glu Thr Leu Glu Ser Phe Ala Thr Val Asp  
 90 95 100

gag gac gag ctc cgg gac gcc gtc agg aag tac ggc gac gtc gac gtc  
 391  
 Glu Asp Glu Leu Arg Asp Ala Val Arg Lys Tyr Ala Ala Gly Thr  
 105 110 115

acg acg gct cct gcc tcg gcg tcc gcc taa ttccaggagat gtgtatgtgt  
 441  
 Thr Thr Ala Pro Ala Ser Ala Ser Ala  
 120 125

gcaaatacg cgcgccacc agtcgtcaat aaataaataa ataaataaataa aaataaataa

501

ataaataaat aaaggccaac gtacgacgac aaatttagtgg cgcgccgggt agtagctagc  
561

agagtatgcg ccgccactgt gtcgatctgc agtttggtcg tttaaaagtg attgttagtgt  
621

gtactatgtt cagctcgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa  
681

aaaaaaaaaa aaaaaaaaaa  
700

<210> 14  
<211> 126  
<212> PRT  
<213> Zea mays

<400> 14

Met Ala Ala Glu Glu Gly Ala Val Ile Ala Cys His Thr Lys Asp Glu  
1 5 10 15

Phe Asp Ala Arg Met Ala Lys Ala Lys Glu Gln Gly Lys Leu Val Val  
20 25 30

Ile Asp Phe Met Ala Pro Trp Cys Ser Gly Cys Gln Met Met Ala Pro  
35 40 45

Val Tyr Ala Asp Cys Ala Ser Lys Tyr Pro Ser Ala Val Phe Leu Glu  
50 55 60

Val Asp Val Asp Glu Leu Leu Glu Val Ala Lys Ile Tyr Gly Val His  
65 70 75 80

Val Met Pro Thr Phe Cys Phe Ile Arg Asn Gly Glu Thr Leu Glu Ser  
85 90 95

Phe Ala Thr Val Asp Glu Asp Glu Leu Arg Asp Ala Val Arg Lys Tyr  
100 105 110

Ala Ala Ala Gly Thr Thr Ala Pro Ala Ser Ala Ser Ala  
115 120 125

<210> 15  
<211> 658  
<212> DNA  
<213> Hordeum vulgare

<220>  
 <221> CDS  
 <222> (52)..(420)  
  
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Met Ala  
1  
  
 gcg tcg gca acg gcg gca gtg gcg gcg gag gtg atc tcg gtc cac  
 105  
 Ala Ser Ala Thr Ala Ala Val Ala Ala Glu Val Ile Ser Val His  
 5 10 15  
  
 agc ctg gag cag tgg acc atg cag atc gag gag gcc aac acc gcc aag  
 153  
 Ser Leu Glu Gln Trp Thr Met Gln Ile Glu Glu Ala Asn Thr Ala Lys  
 20 25 30  
  
 aag ctg gtg att gac ttc act gca tca tgg tgc gga cca tgc cgc  
 201  
 Lys Leu Val Val Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg  
 35 40 45 50  
  
 atc atg gct cca gtt ttc gct gat ctc gcc aag aag ttc cca aat gct  
 249  
 Ile Met Ala Pro Val Phe Ala Asp Leu Ala Lys Lys Phe Pro Asn Ala  
 55 60 65  
  
 gtt ttc ctc aag gtc gac gtg gat gaa ctg aag ccc att gct gag caa  
 297  
 Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Pro Ile Ala Glu Gln  
 70 75 80  
  
 ttc agt gtc gag gcc atg cca acg ttc ctg ttc atg aag gaa gga gac  
 345  
 Phe Ser Val Glu Ala Met Pro Thr Phe Leu Phe Met Lys Glu Gly Asp  
 85 90 95  
  
 gtc aag gac agg gtt gtc gga gct atc aag gag gaa ctg acc gcc aag  
 393  
 Val Lys Asp Arg Val Val Gly Ala Ile Lys Glu Leu Thr Ala Lys  
 100 105 110  
  
 gtt ggg ctt cac gcg gcg cag taa ttacctattt gtgttagtatt  
 440  
 Val Gly Leu His Ala Ala Ala Gln  
 115 120  
  
 cgcctaaata aaattgcgc tcaagaagac tatgaatgct gtgtactgct tgctacttgt  
 500  
  
 tgttggttta tggatactgc gatgcttgc ccaagctgt gtgctttgc atatggtaa  
 560  
  
 ccaaaacagg attgctaaat cttagtcgac tgagattaa ccaagtctta gtcaaagcta  
 620

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tattggcgtg atcttacgta aaaaaaaaaa aaaaaaaaa  
658

<210> 16  
<211> 122  
<212> PRT  
<213> Hordeum vulgare

<400> 16

Met Ala Ala Ser Ala Thr Ala Ala Val Ala Ala Glu Val Ile Ser  
1 5 10 15

Val His Ser Leu Glu Gln Trp Thr Met Gln Ile Glu Glu Ala Asn Thr  
20 25 30

Ala Lys Lys Leu Val Val Ile Asp Phe Thr Ala Ser Trp Cys Gly Pro  
35 40 45

Cys Arg Ile Met Ala Pro Val Phe Ala Asp Leu Ala Lys Lys Phe Pro  
50 55 60

Asn Ala Val Phe Leu Lys Val Asp Val Asp Glu Leu Lys Pro Ile Ala  
65 70 75 80

Glu Gln Phe Ser Val Glu Ala Met Pro Thr Phe Leu Phe Met Lys Glu  
85 90 95

Gly Asp Val Lys Asp Arg Val Val Gly Ala Ile Lys Glu Glu Leu Thr  
100 105 110

Ala Lys Val Gly Leu His Ala Ala Ala Gln  
115 120

<210> 17  
<211> 580  
<212> DNA  
<213> Zea mays

<220>  
<221> misc\_feature  
<223> "n" at position 116, 118, 120, 125, 127, 317, 331, 434, 473, 482, 486, 493, 501, 507, 515, 519, 532, 542, and 579 can be an a, c, g, or t

<400> 17  
tcggatccca caccgaggaa aaggagaaga gagcgagggt cggaataatg gcggccgagg  
60

agggtgccgt gatcgctgtc cacaccaagg acgagttcga cgcccgcatg gccaangncn  
120

aggancnggc aagctggtgg tcatcgactt catggccccc tggcagtg ggtgccagat  
180

gatggccccc gtgtacgcgg actgcgccag caagtaccct tccgcggtct tcctcgaggt  
240

cgacgtggac gaactgctgg aagtgcgaa gatctacggc gtccatgtga tgccgacctt  
300

ctgcttcatc aggaacngcg agacgctcga nagctttgct accgtcgacg aagacgagct  
360

ccgggacgccc gtcaggaagt acgcccgc tggcactacg acgctcctgc ctcggcgtcc  
420

gcctaattca gganatgtga tgtgtagcaa atagcgcgcg cgcaccatcg tcnataaata  
480

antaantaat aantaattaa ntaantnaag ggccncgtnc aacaacaatt tntggccccc  
540

cngtattact acaaatttgc ccccccgtt tcattgcnt  
580

<210> 18

<211> 590

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (60)..(425)

<220>

<221> misc\_feature

<223> "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c,  
g,

or t

<400> 18

gttgcaatna caacgaacag aagctctcga tctcaccgac accgaggaag aagagatca  
59

atg gcg tcc gag cag gga gtc gtg atc gcg tgc cac agc aag gct gag  
107

Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu  
1 5 10 15

ttc gac gcc cac atg acc aag gcc cag gaa gcc ggc aag ctg gtg gtc  
155

Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val  
20 25 30

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atc gac ttc act gcc gcc tgg tgc ggt cca tgc cgc gcc atc gcc cca  
203  
Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro  
35 40 45

ctg ttc gtc gaa cac gcc aag aag ttc act cag gtc gtc ttc ctg aag  
251  
Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys  
50 55 60

gtg gac gtg gac gaa gtg aag gaa gtc acc gcg gcc tac gag gtc gag  
299  
Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu  
65 70 75 80

gcg atg ccg acc ttc cac ttc gtc aag aac ggc aag acg gtc gcg acc  
347  
Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr  
85 90 95

atc gtg ggt gcc agg aag gac gag ctc ctg gcc cag atc gag aag cat  
395  
Ile Val Gly Ala Arg Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His  
100 105 110

gcc gcg cct gcg cct gcg tct gct taaaggagat cagtcgtcgc  
445  
Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala  
115 120

cgtcaataag ggccagcacg tatggctgta aatgttgtcg ttatcagntc tggcttgtc  
505

gtttgtgggc gattgtgaac tagtagtatg tngttctat ccnaagccgg aggcgatctt  
565

aacctggat acttgntgng aaaaa  
590

<210> 19  
<211> 122  
<212> PRT  
<213> Zea mays

<220>  
<221> misc\_feature  
<223> "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c,  
g,  
or t

<400> 19

Met Ala Ser Glu Gln Gly Val Val Ile Ala Cys His Ser Lys Ala Glu  
1 5 10 15

Phe Asp Ala His Met Thr Lys Ala Gln Glu Ala Gly Lys Leu Val Val  
20 25 30

Ile Asp Phe Thr Ala Ala Trp Cys Gly Pro Cys Arg Ala Ile Ala Pro  
 35 40 45

Leu Phe Val Glu His Ala Lys Lys Phe Thr Gln Val Val Phe Leu Lys  
 50 55 60

Val Asp Val Asp Glu Val Lys Glu Val Thr Ala Ala Tyr Glu Val Glu  
 65 70 75 80

Ala Met Pro Thr Phe His Phe Val Lys Asn Gly Lys Thr Val Ala Thr  
 85 90 95

Ile Val Gly Ala Arg Lys Asp Glu Leu Leu Ala Gln Ile Glu Lys His  
 100 105 110

Ala Ala Pro Ala Pro Ala Ser Ala Ser Ala  
 115 120

<210> 20  
 <211> 948  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (3)..(737)

<400> 20  
 cc aag atc ctc acc gag acc gtc acc acc gtc gac ttc tcc gcc cgc  
 47  
 Lys Ile Leu Thr Glu Thr Val Thr Val Asp Phe Ser Ala Arg  
 1 5 10 15

ccc ttc cgt gtc gcc tcc gac acc gtt gtc cac gcc gac tcc gtc  
 95  
 Pro Phe Arg Val Ala Ser Asp Asp Thr Val Val His Ala Asp Ser Val  
 20 25 30

gtc gtc gcc acg ggc gcc gtc gcg cgc agg ctg cac ttc gcc ggc tcc  
 143  
 Val Val Ala Thr Gly Ala Val Ala Arg Arg Leu His Phe Ala Gly Ser  
 35 40 45

gac gcc ttc tgg aac cgg ggc atc tcc gcc tgc gac ggg  
 191  
 Asp Ala Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly  
 50 55 60

gct gcg cct atc ttc cgg aac aag ccc atc gcc gtc gtc gga ggc ggg  
 239  
 Ala Ala Pro Ile Phe Arg Asn Lys Pro Ile Ala Val Val Gly Gly Gly

65

70

75

gac tcc gcc atg gag gag gct aac ttc ctc acc aag tac ggc tcg caa  
 287

Asp Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys Tyr Gly Ser Gln  
 80 85 90 95

gtt tac atc atc cac cgc cgc agc gac ttc cgg gcg tcc aag atc atg  
 335

Val Tyr Ile Ile His Arg Arg Ser Asp Phe Arg Ala Ser Lys Ile Met  
 100 105 110

cag gcg cgc acg ctc tcc aac ccc aag atc aag gtc gtc tgg aac tcc  
 383

Gln Ala Arg Thr Leu Ser Asn Pro Lys Ile Lys Val Val Trp Asn Ser  
 115 120 125

gag gtc gtc gag gcc tac ggc ggt gcg gat ggc ggc cca gtc ggc  
 431

Glu Val Val Glu Ala Tyr Gly Ala Asp Gly Gly Pro Leu Ala Gly  
 130 135 140

gtc aag gtc aag gac gtc acc ggc gag gtc tct gat ctc cag gtc  
 479

Val Lys Val Lys Asp Val Val Thr Gly Glu Val Ser Asp Leu Gln Val  
 145 150 155

gcc ggg ctc ttc ttt gcc atc ggt cac gag ccc gcg aca aaa ttt ctt  
 527

Ala Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu  
 160 165 170 175

gga ggg cag ctc gag ctc gac tct gat ggg tat gtc gtc acc aag ccc  
 575

Gly Gly Gln Leu Glu Leu Asp Ser Asp Gly Tyr Val Val Thr Lys Pro  
 180 185 190

ggt tcc acg cac acc agt gtc cag ggg gtc ttt gca gct ggg gat gtc  
 623

Gly Ser Thr His Thr Ser Val Gln Gly Val Phe Ala Ala Gly Asp Val  
 195 200 205

cag gac aag aag tac cgc cag gcc att act gca gct gga tca ggt tgc  
 671

Gln Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys  
 210 215 220

atg gct gct ctg gat gca gag cac tac ctg cag gag gtt gga gca cag  
 719

Met Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Val Gly Ala Gln  
 225 230 235

gaa ggg aag acc gat tga ctatgtctgg gccaagctgc tcttgggcca  
 767

Glu Gly Lys Thr Asp  
 240

aggaaaactt ctccgaaagc cgctctctag tgggttaaac agcacattat tatttggttt  
 827

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taggcctcaa attacgttac attggaaatt gatttatatg agcgtgcga agcttgtata  
887

cattattcgc attgtttatt actcttagag tcttagtcat taatcacact ttgctaaaaa  
947

a  
948

<210> 21  
<211> 244  
<212> PRT  
<213> Zea mays

<400> 21

Lys Ile Leu Thr Glu Thr Val Thr Val Asp Phe Ser Ala Arg Pro  
1 5 10 15

Phe Arg Val Ala Ser Asp Asp Thr Val Val His Ala Asp Ser Val Val  
20 25 30

Val Ala Thr Gly Ala Val Ala Arg Arg Leu His Phe Ala Gly Ser Asp  
35 40 45

Ala Phe Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly Ala  
50 55 60

Ala Pro Ile Phe Arg Asn Lys Pro Ile Ala Val Val Gly Gly Asp  
65 70 75 80

Ser Ala Met Glu Glu Ala Asn Phe Leu Thr Lys Tyr Gly Ser Gln Val  
85 90 95

Tyr Ile Ile His Arg Arg Ser Asp Phe Arg Ala Ser Lys Ile Met Gln  
100 105 110

Ala Arg Thr Leu Ser Asn Pro Lys Ile Lys Val Val Trp Asn Ser Glu  
115 120 125

Val Val Glu Ala Tyr Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly Val  
130 135 140

Lys Val Lys Asp Val Val Thr Gly Glu Val Ser Asp Leu Gln Val Ala  
145 150 155 160

Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly

Gly Gln Leu Glu Leu Asp Ser Asp Gly Tyr Val Val Thr Lys Pro Gly  
 180 185 190

Ser Thr His Thr Ser Val Gln Gly Val Phe Ala Ala Gly Asp Val Gln  
 195 200 205

Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met  
 210 215 220

Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Val Gly Ala Gln Glu  
 225 230 235 240

Gly Lys Thr Asp

<210> 22  
 <211> 556  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (1)..(336)

<400> 22  
 ggc ggt gcg gat ggc ggc ccg cta gcc ggc gtc aag gtc aag gac gtc  
 48  
 Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly Val Lys Val Lys Asp Val  
 1 5 10 15

gtc acc ggc gag gtc tct gat ctc cag gtg gcc ggg ctc ttc ttt gcc  
 96  
 Val Thr Gly Glu Val Ser Asp Leu Gln Val Ala Gly Leu Phe Phe Ala  
 20 25 30

atc ggt cac gag ccg gcg aca aaa ttt ctt gga ggg cag ctc gag ctc  
 144  
 Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly Gly Gln Leu Glu Leu  
 35 40 45

gac tct gat ggg tat gtg gtg ccc aag ccc ggt tcc acg cac acc agt  
 192  
 Asp Ser Asp Gly Tyr Val Val Pro Lys Pro Gly Ser Thr His Thr Ser  
 50 55 60

gtg cag ggg gtc ttt gca gct ggg gat gtc cag gac aag aag tac cgc  
 240  
 Val Gln Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg  
 65 70 75 80

cag gcc att act gca gct gga tca ggt tgc atg gct gct ctg gat gca

288

Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met Ala Ala Leu Asp Ala  
 85 90 95

gag cac tac ctg cag gag gtt gga gca cag gaa ggg aag acc gat tga  
 336

Glu His Tyr Leu Gln Glu Val Gly Ala Gln Glu Gly Lys Thr Asp  
 100 105 110

ctatgtctgg gccaaagctgc tcttgggcca aggaaaactt ctccgaaagc cgctctctag  
 396

tgggtgtaaac agcacattat tatttggttt taggcctcaa attacgttac attggaaatt  
 456

gatttatatg agcgtgcgca agcttgtata cattattcgc attgtttatt actcttagag  
 516

tcttagtcat taatcacact ttgctaaaaa aaaaaaaaaa  
 556

<210> 23  
 <211> 111  
 <212> PRT  
 <213> Zea mays

<400> 23

Gly Gly Ala Asp Gly Gly Pro Leu Ala Gly Val Lys Val Lys Asp Val  
 1 5 10 15

Val Thr Gly Glu Val Ser Asp Leu Gln Val Ala Gly Leu Phe Phe Ala  
 20 25 30

Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly Gly Gln Leu Glu Leu  
 35 40 45

Asp Ser Asp Gly Tyr Val Val Pro Lys Pro Gly Ser Thr His Thr Ser  
 50 55 60

Val Gln Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg  
 65 70 75 80

Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met Ala Ala Leu Asp Ala  
 85 90 95

Glu His Tyr Leu Gln Glu Val Gly Ala Gln Glu Gly Lys Thr Asp  
 100 105 110

<210> 24  
 <211> 1336

<212> DNA  
<213> Zea mays

<220>  
<221> CDS  
<222> (91)..(1086)

<400> 24

gaactgtaat ttcagatttc agagcgcgca agaaccctct tgaccaccgc cgccgcccgc  
60

gogaagccaa gccaaactga gtaaggcgt atg gag gga tcc gcc gct ccg  
114

Met Glu Gly Ser Ala Ala Ala Pro  
1 5

ctc cgc acg cgc atc tgc atc atc ggg agc ggt ccc gct gcg cac acg  
162

Leu Arg Thr Arg Ile Cys Ile Ile Gly Ser Gly Pro Ala Ala His Thr  
10 15 20

gca gcc atc tac gcg gcc cgc gcg gag ctc aag cct gtg ctc ttc gag  
210

Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys Pro Val Leu Phe Glu  
25 30 35 40

ggc tgg atg gcc aac gac atc gcc gcg ggc ggg cag ctc acc acc acc  
258

Gly Trp Met Ala Asn Asp Ile Ala Ala Gly Gly Gln Leu Thr Thr Thr  
45 50 55

acc gac gtc gag aac ttc ccg ggc ttc ccc aac ggc atc atg ggc gcc  
306

Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Asn Gly Ile Met Gly Ala  
60 65 70

gac ctc atg gac aac tgc cgc gcg cag tcc ctg cgc ttt ggc acc aac  
354

Asp Leu Met Asp Asn Cys Arg Ala Gln Ser Leu Arg Phe Gly Thr Asn  
75 80 85

atc ctc tcc gag acc gtc acc gcc gtc gac ttt tcg gcc tgc cca ttc  
402

Ile Leu Ser Glu Thr Val Thr Ala Val Asp Phe Ser Ala Cys Pro Phe  
90 95 100

cga gtt agt gca gac tcc aca acc gtc ctc gcc gat gcg gtt atc gtt  
450

Arg Val Ser Ala Asp Ser Thr Thr Val Leu Ala Asp Ala Val Ile Val  
105 110 115 120

gcc acg gga gcc gtc gcg cgg cgc ctc cac ttc ccc ggg tcc gat gca  
498

Ala Thr Gly Ala Val Ala Arg Arg Leu His Phe Pro Gly Ser Asp Ala  
125 130 135

tac tgg aac cgc ggc atc tcc gcc tgt gtc tgt gac ggt gcc gcc  
546

Tyr Trp Asn Arg Gly Ile Ser Ala Cys Ala Val Cys Asp Gly Ala Ala

140

145

150

ccc atc ttc cgt aac aag ccc atc gcc gtc ata ggc ggc ggc gac tcc  
 594  
 Pro Ile Phe Arg Asn Lys Pro Ile Ala Val Ile Gly Gly Gly Asp Ser  
 155 160 165  
  
 gct atg gag gag tcc aat ttc ctc acc aag tac ggc tcc cac gtc tac  
 642  
 Ala Met Glu Glu Ser Asn Phe Leu Thr Lys Tyr Gly Ser His Val Tyr  
 170 175 180  
  
 atc atc cac cgc cgc aat acc ttc cgt gct tcc aag atc atg cag gcc  
 690  
 Ile Ile His Arg Arg Asn Thr Phe Arg Ala Ser Lys Ile Met Gln Ala  
 185 190 195 200  
  
 agg gcg ctt gag aac ccc aaa att aag gtc ctc tgg gac tcg gaa gtt  
 738  
 Arg Ala Leu Glu Asn Pro Lys Ile Lys Val Leu Trp Asp Ser Glu Val  
 205 210 215  
  
 gtc gag gcc tat ggc ggc gca aac ggc ggc cca ttg gct ggc gta aag  
 786  
 Val Glu Ala Tyr Gly Gly Ala Asn Gly Gly Pro Leu Ala Gly Val Lys  
 220 225 230  
  
 gtt aag aac cta ctg aat ggt gag gtc tcg gat ctt cag gtg tct ggc  
 834  
 Val Lys Asn Leu Leu Asn Gly Glu Val Ser Asp Leu Gln Val Ser Gly  
 235 240 245  
  
 ctc ttc ttc gcc atc ggg cat gag ccg gcg acc aaa ttc ctg ggc gga  
 882  
 Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu Gly Gly  
 250 255 260  
  
 cag ctt gaa ctc gat tca gat ggt tat gtg gaa acc acc aag cca ggt tcc  
 930  
 Gln Leu Glu Leu Asp Ser Asp Gly Tyr Val Glu Thr Lys Pro Gly Ser  
 265 270 275 280  
  
 act cac acc agt gta aag ggt gta ttt gct gct ggc gac gtg cag gac  
 978  
 Thr His Thr Ser Val Lys Gly Val Phe Ala Ala Gly Asp Val Gln Asp  
 285 290 295  
  
 aag aag tac cgt cag gcc att act gcc gct gga tca ggg tgc atg gct  
 1026  
 Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Met Ala  
 300 305 310  
  
 gca ttg gac gct gag cac tac ctg cag gag atc ggt gca cag gag gga  
 1074  
 Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Ile Gly Ala Gln Glu Gly  
 315 320 325  
  
 aag tct gat tga ctatatttag gtgttagcaac cagcaatcca tcgaatagtc  
 1126

Lys Ser Asp  
330

agttgtcggt gctgaaagcc gctctctgat gcgcgttat gccatgggtt gtcgtgagct  
1186

cacgatttagat atacctgatg atttatgctg ctttagtagca tgctattctt atcgtagga  
1246

tccagaagta tgtctgaact ctgaactatt tactggatac ctattcgtga ttactgcctt  
1306

gaagtttttc cttagatatac aaaaaaaaaa  
1336

<210> 25  
<211> 331  
<212> PRT  
<213> Zea mays

<400> 25

Met Glu Gly Ser Ala Ala Ala Pro Leu Arg Thr Arg Ile Cys Ile Ile  
1 5 10 15

Gly Ser Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala  
20 25 30

Glu Leu Lys Pro Val Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala  
35 40 45

Ala Gly Gly Gln Leu Thr Thr Thr Asp Val Glu Asn Phe Pro Gly  
50 55 60

Phe Pro Asn Gly Ile Met Gly Ala Asp Leu Met Asp Asn Cys Arg Ala  
65 70 75 80

Gln Ser Leu Arg Phe Gly Thr Asn Ile Leu Ser Glu Thr Val Thr Ala  
85 90 95

Val Asp Phe Ser Ala Cys Pro Phe Arg Val Ser Ala Asp Ser Thr Thr  
100 105 110

Val Leu Ala Asp Ala Val Ile Val Ala Thr Gly Ala Val Ala Arg Arg  
115 120 125

Leu His Phe Pro Gly Ser Asp Ala Tyr Trp Asn Arg Gly Ile Ser Ala  
130 135 140

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Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro Ile  
145 150 155 160

Ala Val Ile Gly Gly Asp Ser Ala Met Glu Glu Ser Asn Phe Leu  
165 170 175

Thr Lys Tyr Gly Ser His Val Tyr Ile Ile His Arg Arg Asn Thr Phe  
180 185 190

Arg Ala Ser Lys Ile Met Gln Ala Arg Ala Leu Glu Asn Pro Lys Ile  
195 200 205

Lys Val Leu Trp Asp Ser Glu Val Val Glu Ala Tyr Gly Gly Ala Asn  
210 215 220

Gly Gly Pro Leu Ala Gly Val Lys Val Lys Asn Leu Leu Asn Gly Glu  
225 230 235 240

Val Ser Asp Leu Gln Val Ser Gly Leu Phe Phe Ala Ile Gly His Glu  
245 250 255

Pro Ala Thr Lys Phe Leu Gly Gly Gln Leu Glu Leu Asp Ser Asp Gly  
260 265 270

Tyr Val Glu Thr Lys Pro Gly Ser Thr His Thr Ser Val Lys Gly Val  
275 280 285

Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile Thr  
290 295 300

Ala Ala Gly Ser Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr Leu  
305 310 315 320

Gln Glu Ile Gly Ala Gln Glu Gly Lys Ser Asp  
325 330